

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Fisher, Douglas A.  
Gooding, Douglas H.  
Streeter, David Gray
- (ii) TITLE OF THE INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Dr.
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0442 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 593 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: PROSNOT06
  - (B) CLONE: 828228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Ser	Gly	Ser	Ser	Ser	Tyr	Arg	Pro	Lys	Ala	Ile	Tyr	Leu	Asp
1				5					10					15	
Ile	Asp	Gly	Arg	Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	Tyr	Cys	Asn	Ser
			20					25					30		
Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	Pro	Arg	Asn

		35					40				45				
Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val	Ser	Ile	Asp
	50					55					60				
Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys	Val	Arg	Pro
65					70					75					80
Val	Ala	Ile	Lys	Gln	Leu	Ser	Ala	Gly	Val	Glu	Asp	Lys	Arg	Thr	Thr
				85					90					95	
Ser	Arg	Gly	Gln	Ser	Ala	Glu	Arg	Pro	Leu	Arg	Asp	Arg	Arg	Val	Val
			100					105					110		
Gly	Leu	Glu	Gln	Pro	Arg	Arg	Glu	Gly	Ala	Phe	Glu	Ser	Gly	Gln	Val
		115					120					125			
Glu	Pro	Arg	Pro	Arg	Glu	Pro	Gln	Gly	Cys	Tyr	Gln	Glu	Gly	Gln	Arg
	130					135					140				
Ile	Pro	Pro	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val	Leu	Ala	Gln	Val
145					150					155					160
Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu	Leu	Lys	Ala	Glu
				165					170					175	
Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly
			180					185					190		
Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met
		195				200					205				
Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys
	210					215					220				
Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val
225					230					235					240
Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu
				245					250					255	
Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu
			260					265					270		
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe
		275					280					285			
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp
	290					295					300				
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val
305					310					315					320
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys
				325					330					335	
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His
			340					345					350		
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg
		355					360					365			
Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His
	370					375					380				
His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile
385					390										

[illegible]

## 56

(B) CLONE: 156196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu	Ala	Cys	Phe	Leu	Asp	Lys	His	His	Asp	Ile	Ile	Ile	Ile	Asp	His
1				5					10					15	
Arg	Asn	Pro	Arg	Gln	Leu	Asp	Ala	Glu	Ala	Leu	Cys	Arg	Ser	Ile	Arg
			20					25					30		
Ser	Ser	Lys	Leu	Ser	Glu	Asn	Thr	Val	Ile	Val	Gly	Val	Val	Arg	Arg
		35					40					45			
Val	Asp	Arg	Glu	Glu	Leu	Ser	Val	Met	Pro	Phe	Ile	Ser	Ala	Gly	Phe
	50					55					60				
Thr	Arg	Arg	Tyr	Val	Glu	Asn	Pro	Asn	Ile	Met	Ala	Cys	Tyr	Asn	Glu
65					70					75					80
Leu	Leu	Gln	Leu	Glu	Phe	Gly	Glu	Val	Arg	Ser	Gln	Leu	Lys	Leu	Arg
			85						90					95	
Ala	Cys	Asn	Ser	Val	Phe	Thr	Ala	Leu	Glu	Asn	Ser	Glu	Asp	Ala	Ile
			100					105					110		
Glu	Ile	Thr	Ser	Glu	Asp	Arg	Phe	Ile	Gln	Tyr	Ala	Asn	Pro	Ala	Phe
		115					120					125			
Glu	Thr	Thr	Met	Gly	Tyr	Gln	Ser	Gly	Glu	Leu	Ile	Gly	Lys	Glu	Leu
	130					135					140				
Gly	Glu	Val	Pro	Ile	Asn	Glu	Lys	Lys	Ala	Asp	Leu	Leu	Asp	Thr	Ile
145					150				155						160
Asn	Ser	Cys	Ile	Arg	Ile	Gly	Lys	Glu	Trp	Gln	Gly	Ile	Tyr	Tyr	Ala
			165					170						175	
Lys	Lys	Lys	Asn	Gly	Asp	Asn	Ile	Gln	Gln	Asn	Val	Lys	Ile	Ile	Pro
			180					185					190		
Val	Ile	Gly	Gln	Gly	Gly	Lys	Ile	Arg	His	Tyr	Val	Ser	Ile	Ile	Arg
		195					200					205			
Val	Cys	Asn	Gly	Asn	Asn	Lys	Ala	Glu	Lys	Ile	Ser	Glu	Cys	Val	Gln
	210					215					220				
Ser	Asp	Thr	Arg	Thr	Asp	Asn	Gln	Thr	Gly	Lys	His	Lys	Asp	Arg	Arg
225					230					235					240
Lys	Gly	Ser	Leu	Asp	Val	Lys	Ala	Val	Ala	Ser	Arg	Ala	Thr	Glu	Val
			245					250						255	
Ser	Ser	Gln	Arg	Arg	His	Ser	Ser	Met	Ala	Arg	Ile	His	Ser	Met	Thr
			260					265					270		
Ile	Glu	Ala	Pro	Ile	Thr	Lys	Val	Ile	Asn	Val	Ile	Asn	Ala	Ala	Gln
		275					280					285			
Glu	Ser	Ser	Pro	Met	Pro	Val	Thr	Glu	Ala	Leu	Asp	Arg	Val	Leu	Glu
	290					295					300				
Ile	Leu	Arg	Thr	Thr	Glu	Leu	Tyr	Ser	Pro	Gln	Phe	Gly	Ala	Lys	Asp
305					310					315					320
Asp	Asp	Pro	His	Ala	Asn	Asp	Leu	Val	Gly	Gly	Leu	Met	Ser	Asp	Gly
			325						330					335	
Leu	Arg	Arg	Leu	Ser	Gly	Asn	Glu	Tyr	Val	Leu	Ser	Thr	Lys	Asn	Thr
			340					345					350		
Gln	Met	Val	Ser	Ser	Asn	Ile	Ile	Thr	Pro	Ile	Ser	Leu	Asp	Asp	Val
	355					360						365			
Pro	Pro	Arg	Ile	Ala	Arg	Ala	Met	Glu	Asn	Glu	Glu	Tyr	Trp	Asp	Phe
	370					375					380				
Asp	Ile	Phe	Glu	Leu	Glu	Ala	Ala	Thr	His	Asn	Arg	Pro	Leu	Ile	Tyr
385					390					395					400
Leu	Gly	Leu	Lys	Met	Phe	Ala	Arg	Phe	Gly	Ile	Cys	Glu	Phe	Leu	His
			405						410					415	
Cys	Ser	Glu	Ser	Thr	Leu	Arg	Ser	Trp	Leu	Gln	Ile	Ile	Glu	Ala	Asn
			420					425					430		
Tyr	His	Ser	Ser	Asn	Pro	Tyr	His	Asn	Ser	Thr	His	Ser	Ala	Asp	Val
	435						440					445			
Leu	His	Ala	Thr	Ala	Tyr	Phe	Leu	Ser	Lys	Glu	Arg	Ile	Lys	Glu	Thr
	450					455					460				
Leu	Asp	Pro	Ile	Asp	Glu	Val	Ala	Ala	Leu	Ile	Ala	Ala	Thr	Ile	His
465					470					475					480
Asp	Val	Asp	His	Pro	Gly	Arg	Thr	Asn	Ser	Phe	Leu	Cys	Asn	Ala	Gly
			485						490					495	

Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His  
500 505 510  
His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn  
515 520 525  
Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly  
530 535 540  
Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His  
545 550 555 560  
Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu  
565 570 575  
Glu Asn Gly Glu Thr Asp Lys Asn Gln Glu Val Ile Asn Thr Met Leu  
580 585 590  
Arg Thr Pro Glu Asn Arg Thr Leu Ile Lys Arg Met Leu Ile Lys Cys  
595 600 605  
Ala Asp Val Ser Asn Pro Cys Arg Pro Leu Gln Tyr Cys Ile Glu Trp  
610 615 620  
Ala Ala Arg Ile Ser Glu Glu Tyr Phe Ser Gln Thr Asp Glu Glu Lys  
625 630 635 640  
Gln Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg Asn Thr Cys  
645 650 655  
Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe Ile Thr Asp  
660 665 670  
Met Phe Asp Ala Trp Asp Ala Phe Val Asp Leu Pro Asp Leu Met Gln  
675 680 685  
His Leu Asp Asn Asn Phe Lys Tyr Trp Lys Gly Leu Asp Glu Met Lys  
690 695 700  
Leu Arg Asn Leu Arg Pro Pro Pro Glu  
705 710

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 829179

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln His Gln Thr Asn Pro Gly Gly Pro Thr Asn Arg Arg Arg  
1 5 10 15  
Pro Arg Asp Gln Glu Ile His Gln Glu Pro Arg Tyr Pro Lys Ala Arg  
20 25 30  
Arg His Thr Pro Ala Trp Pro Pro Thr Gln Ser Arg Ser Trp Thr Gly  
35 40 45  
Ala Ser Thr Ser Trp Arg Pro Ser Arg Pro Ile Ala Ala Ser Pro Thr  
50 55 60  
Trp Arg Arg Leu Ser Ser Asn Ala Cys Ser Thr Arg Ser Cys Arg Thr  
65 70 75 80  
Leu Ala Ser Pro Ala Asp Arg Glu Ile Arg Phe Pro Asn Ile Tyr Val  
85 90 95  
Pro His Phe Trp Asp Lys Gln Gln Glu Phe Asp Leu Pro Ser Leu Arg  
100 105 110  
Val Glu Asp Asn Pro Glu Leu Val Ala Ala Asn Ala Ala Gly Gln  
115 120 125  
Gln Ser Ala Gly Gln Tyr Ala Arg Ser Arg Ser Pro Arg Gly Pro Pro  
130 135 140  
Met Ser Gln Ile Ser Gly Val Lys Arg Pro Leu Ser His Thr Asn Ser  
145 150 155 160  
Phe Thr Gly Glu Arg Leu Pro Thr Phe Gly Val Glu Thr Pro Arg Glu  
165 170 175  
Asn Glu Leu Gly Thr Leu Leu Gly Glu Leu Asp Thr Trp Gly Ile Gln

180 185 190  
 Ile Phe Ser Ile Gly Glu Phe Ser Val Asn Arg Pro Leu Thr Cys Val  
 195 200 205  
 Ala Tyr Thr Ile Phe Gln Ser Arg Glu Leu Leu Thr Ser Leu Met Ile  
 210 215 220  
 Pro Pro Lys Thr Phe Leu Asn Phe Met Ser Thr Leu Glu Asp His Tyr  
 225 230 235 240  
 Val Lys Asp Asn Pro Phe His Asn Ser Leu His Ala Ala Asp Val Thr  
 245 250 255  
 Gln Ser Thr Asn Val Leu Leu Asn Thr Pro Ala Leu Glu Gly Val Phe  
 260 265 270  
 Thr Pro Leu Glu Val Gly Gly Ala Leu Phe Ala Ala Cys Ile His Asp  
 275 280 285  
 Val Asp His Pro Gly Leu Thr Asn Gln Phe Leu Val Asn Ser Ser Ser  
 290 295 300  
 Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His  
 305 310 315 320  
 Leu Ala Val Ala Phe Lys Leu Leu Gln Asn Gln Gly Cys Asp Ile Phe  
 325 330 335  
 Cys Asn Met Gln Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile  
 340 345 350  
 Asp Ile Val Leu Ser Thr Asp Met Ser Lys His Met Ser Leu Leu Ala  
 355 360 365  
 Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Ala Gly Ser Gly Val  
 370 375 380  
 Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Glu Asn Leu  
 385 390 395 400  
 Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Pro Leu Tyr  
 405 410 415  
 Lys Arg Trp Val Ala Leu Leu Met Glu Glu Phe Phe Leu Gln Gly Asp  
 420 425 430  
 Lys Glu Arg Glu Ser Gly Met Asp Ile Ser Pro Met Cys Asp Arg His  
 435 440 445  
 Asn Ala Thr Ile Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val  
 450 455 460  
 His Pro Leu Trp Glu Thr Trp Ala Ser Leu Val His Pro Asp Ala Gln  
 465 470 475 480  
 Asp Ile Leu Asp Thr Leu Glu Glu Asn Arg Asp Tyr Tyr Gln Ser Met  
 485 490 495  
 Ile Pro Pro Ser Pro Pro Pro Ser Gly Val Asp Glu Asn Pro Gln Glu  
 500 505 510  
 Asp Arg Ile Arg Phe Gln Val Thr Leu Glu Glu Ser Asp Gln Glu Asn  
 515 520 525  
 Leu Ala Glu Leu Glu Glu Gly Asp Glu Ser Gly Gly Glu Thr Thr Thr  
 530 535 540  
 Thr Gly Thr Thr Gly Thr Ala Ala Ser Ala Leu Arg Ala Gly Gly  
 545 550 555 560  
 Gly Gly Gly Gly Gly Gly Gly Met Ala Pro Arg Thr Gly Gly Cys Gln  
 565 570 575  
 Asn Gln Pro Gln His Gly Gly Met  
 580

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGACAGG GTTGATGCT

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

21

TCGCTTAGTT TTACCGTTTT C

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

22

TATCGCCTCC ATCAACAAAC TT

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

19

GACACAGAAC AGCCACCTC

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

21

AGCAAGTTCA GCCTGGTTAA G

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

24

CTTATGAGTA TTTCTTCCAG GGTA

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCATGGTTA CAAATTATCG AAGCCAATTA

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCCTCCCT CATCTTCTTA

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGACAGCCA AGTGATTT

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCGCTGGCC TTCCTGGTAG

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PF-0442-2 DIV